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                                             Sequence 36, Appl
Sequence 7714, Ap
Sequence 12474, A
Sequence 29, Appl
Sequence 202, Appl
Sequence 21, Appl
Sequence 305, Ap
Sequence 3, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10511, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
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US-09-767-041-41	US-09-925-301-883	US-09-741-669-430	US-10-042-523-4	US-09-934-868-38	US-09-934-899-18	US-09-902-525-46	US-09-900-038A-1	US-09-934-868-32	US-09-934-899-12	US-09-765-272-202	US-09-765-272-198	US-09-816-028A-33	US-10-007-267-12	US-10-007-267-5	US-09-816-028A-34	US-09-738-626-4733	US-09-767-041-47	US-09-765-272-200	US-09-816-028A-29	US-09-816-028A-31	us-09-765-272-196	US-09-738-626-3894	US-09-816-028A-27	US-09-879-959-10	US-10-074-527-4
Sequence 41, Appl		430,	4, 2	38,	Sequence 18, Appl	6	Sequence 1. Appli	32		202	198		12	Sequence 5. Appli	34	Sequence 4733. Ap	Sequence 47. Appl	Sequence 200. App	Sequence 29. Appl	Sequence 31. Appl	Sequence 196. Ann	894	27	Sequence 10, Appl	Sequence 4 Appl

ALIGNMENTS

닭 ρ 밁 QΥ 망 Q ; FEATURE: ; NAME/KEY: misc_feature ; OTHER INFORMATION: CPS1K US-09-767-041-36 RESULT 1 US-09-767-041-36 Query Match Best Local Similarity SOFTWARE: PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0 Matches GENERAL INFORMATION: Sequence 36, Sequence 36, Application US/09767041 Patent No. US20020055168A1 TITLE OF INVENTION: STREPFOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS FILE REFERENCE: 2183-4726 CURRENT APPLICATION NUMBER: US/09/767,041 CURRENT FILING DATE: 2001-01-22 NUMBER OF SEQ ID NOS: TITLE OF INVENTION: APPLICANT: TYPE: PRT
ORGANISM: Streptococcus suis LENGTH: 122 DRVDASGHFLTAEPLPTN----110 LGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC-----HQSI-----FYRR 156 62 IRYFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGY 121 62 LVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLY------EPTTLAQVAAF 109 3 TISKISIIVPIYNVEKYLSKCIDSIVNQTYKHIETLLVNDGSTDNSEEICLAYAKK-DSR 61 2 TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR 61 PatentIn version 3.0 Smith, Hilda Conservative 12.8%; Score 179; DB 10; 23.6%; Pred. No. 3.6e-11; rative 47; Mismatches 93; 1998-07-22 1998-07-22 1999-07-19 EP98202467.1 EP98202465.5 PCT/NL99/00460 ---QAVLSGRNVCKKLLEADGHRFVVACNKLYKK 170 Length 278; Indels 58; Gaps 10;

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LENGTH: 332
TYPE: PRT
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Best Local S
Matches 68
Sequence 5714, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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PRIOR FILING DATE: 1998-07-22
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PRIOR FILING DATE: 1999-07-19
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CURRENT FILING DATE: 2001-01-22
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mes 68; Conserv
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o. US20020055168A1
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Pred. No. 5.9e-11;
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; ORGANISM: Staphylococcus aureus US-09-815-242-5714
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SEQ ID NO 5714
LENGTH: 358
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12474, Application US/09815242
                                                          CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                           APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
                      PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                           FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
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APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLETNSG---GPGKPRNVALKQAEGEFVLFVDSDDYI-NKETLKDAAAFIDEHHSDVLL- 115
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                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                Carr, Grant
                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr, Grant
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Wall, Daniel
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Pred. No. 2.9e-10;
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                                                                                                                                                   Essential Genes
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; OTHER INFORMATION: Consensus amino acid
US-09-924-358-29
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US-09-815-242-12474
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 150
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APPLICANT: MacBeth, Kyle
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 80764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 38155-20034.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version EQ ID NO 12474 LENGTH: 573
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 QLETNSG---GPGKPRNVALKQAEGEFVLFVDSDDYI-NKETLKDAAAFIDEHHSDVLL- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                          60 LEENLGLAAARNAGLKHATGDYDYIAFLDADDEV--PDWLEKLLELLEKNGAD-IVIGRV 116
                                                                                    66
                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FSVIVPTYNSEKYITELLNSLAKODFPKTEFEVVVVDDCSTDQTLQIVEKYRNKLNLKVS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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VMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFD 160
                                                                                                                                                           SIIIPTFNAAVTLQACLGSIVGQ-TYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVH 65
                                                                             SGPDDGPYDAMNRGVGVATG--EWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
                                                                                                                        SIIIPTYNEEKYLEECLESLLNQTTYENFEIIVVDDGSTDGTVEILEEYAKDPRIR-VIR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --IKMKGVNGRGVPQSMFKETAPEVTLLNSRIIY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29, Application US/09924358
5. US20020107376A1
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                                                                                                                                                                                                          Conservative
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BER: US 60/229,300
                                                                                                                                                                                                     11.8%; Score 165.5; DB 10
35.0%; Pred. No. 4.3e-10;
tive 26; Mismatches 63;
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Mismatches
                                                                                                                                                                                                                                             DB 10;
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RESULT 7 US-09-767-041-21

GENERAL INFORMATION:

APPLICANT:

Smith, Hilda

CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22

2183-4726

STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS

PRIOR APPLICATION NUMBER:

PCT/NL99/00460

TITLE OF INVENTION: FILE REFERENCE: 2:

Sequence 21, Application US/09767041 Patent No. US20020055168A1

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LENGTH: 251
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213 ALMGVRQSFIRLVRGFYTIK--IAWKREPVHQRLESR 247
                                                                                                                                                                111 ETPGRTIVALTGT---GSFDIPGRMGEWLALCYLGA-YRWSTKQALGHYPI-----
                                                                                                                                                                                                      118 LYYGDVVMRSTKSRHAGPFDLDRLLFE-TNLCHQSIFYRRELFDGIGPYNLRYRVWADWD 176
                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 76; Conserv
                                                                                                                                                                                                                                                                                                                              1 MTTSIQRRISIVIPCLNDAVLLEQCLSSIVAQTLQPEEVIVVDNGSTDNSVEVAN----R
                                                                                                                                                                                                                                                                                                                                                                    1 MTAPV---FSIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPE 57
                                                                                                                       FNIRCESNPALITRYM------DVVISE----YNDM-TGESMRQGTDKEFRKRLPMYF---
                                                                                                                                                                                                                                               MGAR-VVHE-PLQGITWASAAGYNSARGDLIVRFDA-DCVIPPDHLSQVNAIWN---RTE 110
                                                                                                                                                                                                                                                                                   LGSRLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/738,626
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                 -FGSNSVISRQWWEDVKDQITLSETFVHEDMYFSFFVRPHETVWFEKNLKLIMHPR 212
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                          -WVAGWETCRRMLAFLKDKENRRLALR 249
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                                                                                                                             US-09-738-626-3905
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                                                                                                                                                                      SOFTWARE: Pate
SEQ ID NO 3905
LENGTH: 274
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 21
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE:
                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 332
TYPE: PRT
                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: CPS2J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ience 3905, Application US/09738626
ication No. US20020197605A1
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                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GPDDGPYDAMNRGVGVATGEWVLFLGADD-----TLYEPTTLAQ------VAAF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LPNGGVSNARNYGIKNSTANYIMFVDSDDIVDGNIVESLY--TCLKENDSDLSGGLLATF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                             2 TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP9
FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIIVPIFNTEKYLRECLDSIISQSYTNLEILLIDDGSSDSSTDICLEYAEQDG-RIKLFR 63
SAPLISVVIPTIAYDEYCSQSIKSVCEQNYENWQIVLVLDGAPIK--DVPQWVKEH--ER 59
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/738,626
                                                                                                                                                                                                          PatentIn ver.
                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                            YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                              OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAYASHI,
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                                                                                                                                                                                                                                                                                                                                                                                                                IKEDA, MASATO
                                                               Conservative
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                                                                                             Score 162.5;
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Pred. No. 2.4e-09;
                                                                            Pred. No. 2.1e-09
                                                               Mismatches
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                                                                                           DB 9;
                                                               108;
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                                                              Indels
                                                                                        Length
                                                                                             274;
                                                              41;
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                                                            Gaps
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; OTHER INFORMATION: N-terminal part of CPS2J
US-09-767-041-51
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US-09-767-041-51
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                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                            Sequence 3, Application US/10007267
Patent No. US/20020127/682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/0046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER: EPPLICATION NUMBER: 1998-07-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 NLRYRVWADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 --IICVATKTKHINEHGKIFGQSADLPTSQDIRQILLVKNPIIHSSVMYRKQVVEQIGGY
                                                                                                                                                                                                                                                                                                               64 LPNGGVSNARNYGIKNSTANYIMFVDSDD 92
                                                                                                                                                                                                                                                                                                                                                 67 GPDDGPYDAMNRGVGVATGEWVLFLGADD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60. IKIVEQKIRQGTPTSLNNGIKASDGQLIARLDSDD-LAAPSRLSKQEEFLRNHPY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 L-VVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                                                                                                                                                                                                                                                                                                                                                                                                              7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                                                                                                                                                                                                                                                           5 SIIVPIFNTEKYLRECLDSIISQSYTNLEILLIDDGSSDSSTDICLEYAEQDG~RIKLFR 63
                                                                            NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                      APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGWETCRRM--LAFLKDKENRRLAL 248
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                                                            ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, Hilda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                      Hackensack
New Jersey
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                                      411 Hackensack Avenue
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                                                                                                                    OLIGOSACCHARIDES,
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                    AND GENES ENCODING THEM
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COUNTRY: USA

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RESULT 11
US-10-007-267-11
                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LAQAQNSGLIPSINIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD------TLYEPTTLAQ 105
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 201 487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLYSYLICAYNYEKYFAQSLAAVVNQTWRNLDILIYDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                    COUNTRY: USA
ZIP: 07601
                                                                                                                           STATE: New Jersey
                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                 CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
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                                                                                                                                                                                                                                                                        INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
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                                                                                                                                                                                                                                                  OLIGOSACCHARIDES, AND GENES ENCODING THEM
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Pred. No. 8.9e-09;
7; Mismatches 80;
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2000-05-26

60/207,727

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Query Match
Best Local Similarity
Matches 47; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4950, Application Patent No. US20020061569A1
                                       FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-05
                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                     APPLICANT:
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF --- FPFGNPIHNNTMIMRRS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 LFDGIGPYNLRYRVWADW 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/333,412 FILING DATE: 15-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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                                                                                                                                                                                                    Xu, H. Howard
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Yamamoto, Robert T.
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2000-05-23
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                     60/206,848
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Pred. No. 8.9e-09;
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LENGTH: 706
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Best Local Similarity
                                                                                                                     PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                SOFTWARE:
                                                                                                       PRIOR FILING DATE:
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                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                    RIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: Identification of Essential Genes ITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 DLIYSDEDKIDMDGNRSDPAFKPDWSPDLLLGTNYISHLGVYRRSILEEIGGFRKGYEGS
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                       FILING DATE: 2000-11-27
                                                                                                                                                                                                        APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-05-23
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                                                           FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, H. Howard
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Zyskind, Judith W.
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26.1%;
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Pred. No. 2.7
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 54; Conserv
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SEQ ID NO 39
LENGTH: 270
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Patent No. US20020042369A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/118,213 PRIOR FILING DATE: 1999-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Campylobacter Glycosyltransferases TITLE OF INVENTION: Gangliosides and Ganglioside Mimic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                   183 SNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFW----VAGWETC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 QDYDLVLR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 HLVYGD----VVMRSTKSRHAGPFDLD-RLLFETNLCHQSIFYRRELFDGIGPYNLRYRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 PKISIAMPYYNVEEKWLRLCIDSILNQVYTNWELCMADDASTDPNVKKILTEYQQLDERI 241
162
                                                                            118 AFVHRVKTKQFYRFKQD-----
                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 DLIYSDEDKIDMDGNRSDPAFKPDWSPDLLLGTNYISHLGVYRRSILEEIGGFRKGYEGS
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                                                                                                                                                                                                                                                                              4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/495,406 FILING DATE: 2000-01-31
KKDIILKSFEKIKIDE----
                                                                                                                                                                                                                                      PQLSITIPLENSCOFISRALQSCINQTLKDIEILIIDDKSKDNSLNMYLEFAKK-DPRIK 60
                                                                                                                VVMRSTKSRHAGPEDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIRCF
                                                                                                                                                       IFQNEENLGTFASRNLGVLHSSSDFIMFLDSDDFL---TPDACEIAFKEMKKGFDLLCFD
                                                                                                                                                                                             VHSGPDD-GPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGD 122
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                                                                                                                                                                                                                                                                                                                   Conservative
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26.1%;
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-RLNYGEDVLF - - - CYTYFMFCEKIAVFKTC
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Pred. No. 9.1e-09;
8; Mismatches 96;
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Pred. No. 2.7e-08;
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                                                                            -EVFNQKEFLEFLS--KQRHFCWSVW---AKCF
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204
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US-09-767-041-52

Sequence 52, Application US/09767041
Patent No. US/0020055188A1

GENERAL INFORMATION:
APPLICANT: SMITCH, Hilda
TITLE OF INVENTION:
APPLICANTION STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REFERENCE: 2189-4726

CURRENT PAPLICATION NUMBER: D909/767,041

CURRENT PAPLICATION NUMBER: D909/769.

PRIOR APPLICATION NUMBER: EP98202465.5

PRIOR APPLICATION NUMBER: EP98202467.1

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4, Appli 2, Appli 2, Appli 2, Appli 4067, Ap 168, App 168, Appli 4, Appli 10, Appli

Sequence Sequence Sequence Sequence

5, Appli 5, Appli 12, Appli 5, Appli 4051, Ap 198, App 202, App 5633, Ap

Sequence Sequence Sequence

5, Appli

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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
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/cgn2_6/ptodata/1/iaa/BC_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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first 45 summaries
                                      1 US-08-597-236-10
US-08-746-682A-10
US-08-312-387B-11
US-08-683-426-3
US-08-683-426-3
US-08-683-426-11
US-08-683-426-11
US-08-683-426-11
US-08-683-458-11
US-08-878-360-11
US-08-478-140B-3
US-08-478-140B-3
US-08-478-140B-3
US-08-478-140B-3
US-08-478-140B-8
US-09-338-943-3
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US-08-683-426-5
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       Sequence 10, Appl Sequence 3, Appli Sequence 3, Appli Sequence 11, Appl Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 11, Appli Sequence 1, Appli Sequence 5, Appli Sequence 12, Appli S
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Patent No. 5733765
Patent INFORMATION:
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US-08-597-236-10
                                                                                                                                                                       Matches
                                                                                                                                                                                             Query Match
Best Local :
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CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FABUCCI A., Alan
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 3
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/597,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STINGELE, Fr. APPLICANT: MOLLET, Beat TITLE OF INVENTION: LAC'TITLE OF INVENTION: EXO
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ADDRESSEE: Pennie & Edmonds
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65 HSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYG
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 10036
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                                                                                                           5 VFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVV 64
                                                              LISIVIPVYNVEKYLEKCLOSVONOTYNNFEVILVNDGSTDSSLSICEKFVNO-DKRFSV 64
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5. 5733765
                                                                                                                                                                     l Similarity
42; Conserv
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US-08-878-360-12
US-08-478-140B-5
US-09-333-412-12
US-09-333-412-12
US-09-3314-001C-4051
US-09-314-001C-4051
US-08-961-083-202
US-09-134-001C-5633
US-08-270-581-2
US-09-134-001C-4067
US-08-961-083-168
US-08-961-083-168
US-08-961-083-168
US-08-961-083-168
US-08-960-048-9
US-08-960-048-9
US-08-960-048-9
US-08-960-048-9
US-08-960-048-9
US-08-960-048-9
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Pred. No. 2e-10;
                                                                                                                                                                  Mismatches
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Query Match

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Title: Perfect score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                      Sequence 3, Application US/08312387B Patent No. 5545553
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gotsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: CFILING DATE: 20-JUN-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                       CITY:
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                                                     STREET:
                                                                    ADDRESSEE:
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                                  Hackensack
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                                                   411 Hackensack Avenue
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                                                                                                                                      Gotschlich, Emil C.
VENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                      OLIGOSACCHARIDES,
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Pred. No.
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                                                                                                                      AND GENES ENCODING THEM
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Best Local S
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TELEPHONE: 201 487-5800
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                  APPLICATION NUMBER: FILING DATE: July
                                                                                                                                                                                      COUNTRY:
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                   CLASSIFICATION:
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Similarity 23.7%;
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                                                                                    Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                              Gotschlich, Emil C.
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N: 435
INFORMATION:
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                            July 7, 1994
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                                                                                                                                                                                                                                                                                                              OLIGOSACCHARIDES,
                                                                                                                                                                                                                                                                                                                                GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
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Pred. No. 4.9e-10;
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                                                                                       Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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LENGTH: 348 amino acid
                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: Septembe
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                TELECOMMUNICATION INFORMATION:
                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
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                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                        FILING DATE:
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              TELEPHONE:
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                                                                                                                                NUMBER: 08/312,387
September 26, 1994
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343-1684
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23.7%;
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                                                   600-1-095B
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Pred. No. 4.9e-10;
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Best Local Similarity
"Arches 47; Conserve
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Sequence 11, APE-
Sequence 10, APE-
-08-000
                                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                  SEQUENCE CHARACTERISTICS
                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                              TELEFAX:
                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                    LENGTH:
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: 348 amino acids
amino acid
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SYSTEM: PC-DOS/MS-DOS
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GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                        Release #1.0, Version
                                                                                                                                                                                                                                                                             US/08/683,426
                                                                                                                                                                                                                   08/312,387
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Pred. No. 4.9e-10
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JS-08-683-426-11

MOLECULE TYPE:

TOPOLOGY:

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Best Local Similarity
Watches 47; Conserve
                                                                                                                                   US-08-683-458-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683.450
FILING DATE:
CLASCITATE:
                                                         Query Match 11.3%;
Best Local Similarity 23.7%;
Matches 47; Conservative 37
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                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%; Score 158; DB 1; Length 348; 23.7%; Pred. No. 4.9e-10;
                                                         ; Score 158; DB 1; Length 348; ; Pred. No. 4.9e-10; 37; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                             600-1-095A
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                                                       Gaps
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157	106 VAAFLGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE	δõ
122	63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA	₽
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ω	4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSERPELGSRLV 6	γQ
š 5;	Query Match 11.3%; Score 158; DB 1; Length 348; Best Local Similarity 23.7%; Pred. No. 4.9e-10; Matches 47; Conservative 37; Mismatches 80; Indels 34; Gaps	
	MOLECULE TYPE: protein 9-08-683-458-11	us ;
	LENGTH: 348 amino acids TYPE: amino acid TOPOTOCY: linear	
	TELEX: 133521 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:	
	N INFORMATION: 1 487-5800 343-1684	
	REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095A	
•	FORMATION:	
	: Septemb	
	08/312	
	4. 7.	
	4 58	·· ··
	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	·· ··
	ZIP: 07601 COMPUTER READABLE FORM:	٠. ٠.
	方	٠. ٠.
	Hackensack	
	ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue	
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	TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM	
	INFORMATION: CANT: Gotschlich, Emil C.	٠. ٠.
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	5 179 VIDGGLRYDTERDW 192	D D
	158 LFDGIGPYNLRYRVWADW 175	Qy
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157	106 VAAFLGDHAASHLVYGDVVMRSTKSRHAGDFDLDRLLFETNICHQSIFYRRE	Qy
122	63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA	Дb
105	64 VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQ	Qy
62	3 PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI	망

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RESULT 9 US-08-878-360-3

Sequence 3, Application US/08878360 Patent No. 5945322

GENERAL INFORMATION:

Gotschlich,

Emil C.

NUMBER OF SEQUENCES: 1 TITLE OF INVENTION:

ADDRESSEE

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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                               123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
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                                                                                                                                        63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                               64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
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                                                                                                                                                                                                                      PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                      ----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
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Pred. No. 4.9e-10;
7; Mismatches 80;
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RESULT 11
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Best Local Similarity
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US-08-878-360-11
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LENGTH: 348 amino acids
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CORRESPONDENCE ADDRESS:
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                                                                                                                      158 LFDGIGPYNLRYRVWADW 175
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                                                                                                                                                                                                                                         63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                           64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD------TLYEPTTLAQ 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                               VIDG----GLRYDTERDW
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                                                                                                                                                                                                                                                                                                                                                                                                Score 158; DB 2;
Pred. No. 4.9e-10;
7; Mismatches 80;
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158 LFDGIGPYNLRYRVWADW 175

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Query Match Best Local Similarity "-+-hes 47; Conserv

Conservative

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-878-360-3

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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TELEFAX:

201 343-1684

LENGTH:

amino acid

348 amino acids

APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

08/683,426

FILING DATE:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

New Jersey

411 Hackensack Avenue

Klauber & Jackson

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                                                                                 Sequence 8, Application US/08478140B Patent No. 6127153
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                                                                 GENERAL INFORMATION:
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 TITLE OF INVENTION:
                    APPLICANT:
                                  APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                       106 VAAFL-----
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                                                                                                                                                                                                                                                                                                                                                   64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
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BUCZALA, STEPHANIE L.

/ENTION: METHOD OF TRANSFERRING AT LEAST TWO
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BUCZALA, STEPHANIE L.
                                JOHNSON, KARL F.
ROTH, STEPHEN
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SYSTEM: PC-DOS/MS-DOS
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A. Coruzzi
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23.7%; Pred. No. 4
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of the Americas
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TITLE OF INVENTION:

OLIGOSACCHARIDES,

GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS

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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

STREET: 411 Hackensack Avenue ADDRESSEE: Klauber & Jackson

Hackensack

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                                                                                           RESULT 13
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Sequence 3, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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NAME: Laura A. Coruzzi
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MEDIUM TYPE: Floppy disk
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                                                                                                                                            179 VIDG----GLRYDTERDW
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                                                                                                                                                                                                                                                 106 VAAFL------GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
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                                                                                                                                                                                                                                                                                                                      64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----TLYEPTTLAQ 105
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SOFTWARE: Patentin
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 158; DB 3; 23.7%; Pred. No. 4.9e-10; tive 37; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                      US-09-333-412-11
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GENERAL APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYTARTDADDIASPGWIEKIVGEMEKDRSIIA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHSGPDDGPYDAMNRGV------GVATGEWVLFLGADD------TLYEPTTLAQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 47; Conserv
                                                                                                                     COUNTRY: USA
                                                                                                                                        STATE: New Jersey
                                                                                                                                                           CITY: Hackensac
                                                                                                                                                                                  STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     ZIP: 0760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343-1684
                                                                                                                                                                                                                                                              GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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US-09-338-943-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6379933
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TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO: 11:
CURRENT APPLICATION DATA:
                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VIDG----GLRYDTERDW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VHSGPDDGPYDAMNRGV-----GVATGEWVLFLGADD-----
                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                               STATE:
                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09338943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/312,387 FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-Jun-1999
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                                                                                                                                                             New York
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                                                                                                                                                                                                   1155 Avenue
                                                                                                                                                                                                                                                                                                                                                               BUCZALA,
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                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                      Pennie &
                                                                                                                                                                                                                                                                                                                                                                                    STEPHEN
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METHOD OF TRANSFERRING AT LEAST TWO
SACCHARLDE UNITS WITH A POLYGLYCOSYLTRANSE
POLYGLYCOSYLTRANSFERASE AND GENE ENCODING
                                                                                                                                                                                                                                                                                 POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                     of
                                                                                                                                                                                                   the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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                                                                                                                                                                                                                                                                                                                       POLYGLYCOSYLTRANSFERASE,
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-338-943-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
179 VIDG----GLRYDTERDW 192
                                                                                     123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAF----FPFGNPIHNNTMIMRRS 178
                                          158 LFDGIGPYNLRYRVWADW 175
                                                                                                                                  106 VAAFL-----GDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRE 157
                                                                                                                                                                             63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                        64 VHSGPDDGPYDAMNRGV------GVATGEWVLFLGADD------TLYEPTTLAQ 105
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                                                                                                                                                                                                                                                                     7188-017
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Search completed: April 17, 2003, 17:29:27 Job time: 30 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB seq
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Perfect score:
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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093025
098520
08VIX0
                                                                   Q8VL41
Q9EXY1
Q8VTW8
                                          Q9EXY4
Q9ZGK3
                                                                                                                         Q9AEE4
Q8VTX7
Q8VTW5
  Q9S4F9
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093q25 salmonella
09s520 escherichia
08vtx0 leptospira
09aee4 leptospira
Q9zgk3 leptospira
Q9exz1 salmonella
Q9s4f9 leptospira
Q9exy9 salmonella
                                                     Q8vtw8 leptospira
Q9exy4 escherichia
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	Q9S4F8	Q8TN31	Q9ALX0	086296	Q93DZ7	Q92GK2	Q915M1	P95448	097н38	Q8YW50	085336	Q8YSL7	Q97Н39	Q92V61	Q8YYD6	Q9LA88	Q9AFH3	Q8YSM1	Q9UZI6	Q8YSL6	Q98JH2	Q8YSM2	Q8YSL1	024928		Q9RCC4	_	Q9RQ94	Q9XDJ3
	Q9s4f8 leptospira	Q8tn31 methanosarc	Q9alx0 streptococc		Q93dz7 streptococc	سر	Q915ml pseudomonas	ъ			O85336 escherichia			rhizobium	on.		ω		-		Q98jh2 rhizobium l	anabaena		-	helicobac	4 yersinia	_		Q9xdj3 bacteroides

ALIGNMENTS

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES-M.avium; STRAIN-TMC 724; Eckstein T.M., Brennan P.J., Inamine J.M., Belisle J.T.; Eckstein T.M. of gene cluster involved in glycopeptidolipid biosynthesis and of a gene cluster encoding daumorubicin resistance in two strains of Mycobacterium avium serovar 2.";	[2] SEQUENCE FROM N.A. SPECIES-M. avium; STRAIN-2151; SPECIES-M. j. Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.; Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.; "Identification of a gene cluster involved in glycopeptidolipid biosynthesis and of a gene cluster encoding daunorubicin resistance in two strains of Mycobacterium avium serroyar 2."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES-M.avium subsp. silvaticum, and M.paratuberculosis; Tizard M., Bull T., Millar D., Doran T., Martin H., Ford J., Hermon-Taylor J.; Hermon-Taylor J.; A low G+C content element in Mycobacterium avium subsp. Paratuberculosis and M. avium subsp. silvaticum with homologous genes in M. tuberculosis. T. Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.	GSD OR GTED. GSD OR GTED. Mycobacterium avium subsp. silvaticum, Mycobacterium paratuberculosis, and Mycobacterium avium. Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID-44282, 1770, 1764;	ILT 1 .09 .081.09 PRELIMINARY; PRT; 266 AA. O881.09; O1-NOV-1998 (TremBLrel. 08, Created) O1-NOV-1998 (TremBLrel. 08, Last sequence update) O1-UN-2001 (TremBLrel. 17, Last annotation update) GEN protein

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Best Local S
Matches 266
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Wang L., Reeves P.R.;

"The E. coli Oll1 and S. enterica 035 gene clust."

encoding the same colitose containing 0 antigen conserved.";

conserved.";

submitted (JUL-2000) to the EMBL/GenBank/DDBJ da EMBL; Ar285969; AAK83018.1; -

InterPro; IPR001173; Glycos_transf_2.

Pfam; PF00535; Glycos_transf_2; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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SEQUENCE :
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L; AJZ23832; CAA11578.1; -.

L; AJZ23833; CAA11578.1; -.

L; AF143772; AAD44222.1; -.

L; AF125999; AAD20376.1; -.

erPro; IPR001173; Glycos_transf_2.

m; PF00535; Glycos_transf_2; 1.
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                                                                                       CFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRRMLAFLKD
                         VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
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IVSEKDRGIYDAWNKAVDLSSGDWIAFIGSDDVYYHTDAITSLVKGAAISNGAPVVYG--
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Last annotation update)
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Pred. No. 4.2e-18;
Pred. No. 4.2e-18;
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Pred. No. 1.2e-114;
; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                "Sequencing of Escherichia coli Olli O-antigen identification of Oll1-specific genes.";
J. Clin. Microbiol. 36:3187(1998).
EMBL; APO78736; AAD46731.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, La
01-JUN-2001 (TrEMBLrel. 17, La
Putative glycosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=STOKE W;
MEDLINE=98449835; PubMed=9774562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of Escherichia coli Olll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96060831; PubMed-7590310; Bastin D.A., Reeves P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-STOKE W;
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                                               239
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                                                                                                       FDGIGPYNLRYRVWADWDFNIRCF-----SNPALITRYMDVVISEYNDM-TGFSMRQGT
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27.7%;
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Hypothetical
SEQUENCE 26
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21; La
Hypothetical 31.4 kDa protein.
                                                                                               de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LPS biosynthetic loci of Leptospira interrogans and Leptospira borgpetersenii."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              and transfer genes of the lipopolysaccharide-related Leptospira interrogans serovar Copenhageni.";
J. Bacteriol. 179:1262-1267(1997).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE~97175555; PubMed=9023210; Mitchison M., Bulach D.M., Vinh T.,
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                       SEQUENCE FROM N.A. STRAIN-AKIYAMI A;
                                                                                                                                                                                                       STRAIN-L45;
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MEDLINE-21369626; PubMed-11476985;
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RA de la Pena-Moctezuma A., Bulach D.M., Adler B.;
RT "Genetic differences among the LPS biosynthetic loci of ser.
Leptospira interrogans and Leptospira borgpetersenii.";
RL FEMS Immunol. Med. Microbiol. 31:73-81(2001).
DR EMBL; AF316500; AAL49428.1;
DR Pfam; PF00535; Glycos_transf_2.
TR Pfam; PF00535; Glycos_transf_2; 1.
W Hypothetical protein.______.
SEQUENCE 265 Aa. ...
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 31.4 kDa protein.
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"Genetic differences among
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Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein.
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                                                                              de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LPS biosynthetic loci Leptospira interrogans and Leptospira borgpetersenii. FEMS Immunol, Med. Microbiol. 31:73-81(2001).
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"Genetic differences among the LPS biosynthetic loci Leptospira interrogans and Leptospira borgpetersenii. FEMS Immunol. Med. Microbiol. 31:73-81(2001).
EMBL; AF316564; AAL49462.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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265 AA;
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de la Pena-Moctezuma A., Bulach D.M., Adler B.;
"Genetic differences among the LPS biosynthetic loci
Leptospira interrogans and Leptospira borgpetersenii.
FEMS Immunol. Med. Microbiol. 31:73-81(2001).
EMBL; AF31656; AAL49460.1; -.
EMBL; AF316556; AAL49446.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SALINEM, BALLICO, SWART, AN MEDLINE-21369626; PubMed-11476985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 31.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                      4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTD-----RTLDIANSFRP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTA--PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTD-----RTLDIA 51
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                                                  ADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSM----RQGTDKEFRKRLPMYF
                                                                                                                                                    HLVYGDVVMRSTKSRHAGPEDLDRLLE----ETNLCHQSIEYRRELEDGIGPYNLRYRVW
                                                                                                                                                                                                                                                                                                      PKISIITINLNNLEGLRKTLESVKSQTYTNFELIVVDGGSTDGSFEYLKSNLDLIKKFIS
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  ADFEFFHRFWFNKNIKIKHASVFVTLY-DFNGVSAQPKNRKRIAEEYQKIKKKYF
                                                                                                    DLVYGNILIDSKUNGIIERKYPDRLNYFYWSIKSLCHQAVFIRKSLFDLYGYYNEEYLFA
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                                                                                                                                                                                                      KDKGIYNAQNKGILLSKGEYLVFLNAGDTLLQKNILLEISKFLDQDV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leptospiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 271; Db .,
Pred. No. 9.3e-16;
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Pred. No. 5.1e-16;
0; Mismatches 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E5539162FA877A9D CRC64;
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227
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Best Local
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     Query Match
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248 AA;
                                                                                                                                                                   de la Pena-Moctezuma A., Bulach D.M., Adler B.; "Genetic differences among the LPS biosynthetic loci of Leptospira interrogans and Leptospira borgpetersenii."; FEMS Immunol Med Microbiol. 31:73-81(2001).
                                                                                                                                                                                                                                                                                                                                                                                        Leptospira interrogans.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira
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01-MAR-2002 (TrEMBLre1. 20, Last sequence update)
01-UN-2002 (TrEMBLre1. 21, Last annotation updat
Hypothetical 31.4 kDa protein.
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Pfam; PF00535; Glycos_transf_2; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
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                                                                        Pfam; PF0053
Hypothetical
                                                                                                                                            FEMS Immunol. Med. Microbiol. EMBL; AF316561; AAL49456.1; -.
                                                                                                                                                                                                                                                                                                   STRAIN-MWOGOLO;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                        InterPro; IPR001173; Glycos_transf_2.
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                                                                                                                                                                                                                                                                     MEDLINE-21369626; PubMed-11476985;
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| crobiology 147:599-610(2001).
| BBL; AX012190; AAG41755.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV-VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIITYTYNSEKTLRDTLESIELQTYKDIEYIIIDGGSTDNTLKLIN----EVSTRVTKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRILKRDDIKVIYVPQV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEKNQIDIIKRYWRSGPFKRSKLSLGWAPPHPSFYMRRELYKDDGYFDLSYRIAADYDOM 178
                                                                                       PF00535; Glycos_transf_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
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                                                    265 AA;
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                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transferase.
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                                                    31442 MW;
     19.18;
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Pred. No. 1.
     Score 267
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                                               A39258BFA6388DAA CRC64;
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RESULT 12
Q9EXY4
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                                                                                                                                                                                                                                              Transferase.
SEQUENCE 2
                                                                                                                                                                                                                                                                  EMBL; AY012189; AAG41752.1; -
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                              Jensen S.O., Reeves P.R.; Molecular evolution of the GDP-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                      in Salmonella enterica.";
Microbiology 147:599-610(2001).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21135136; PubMed=11238967;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-M1182;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative glycosyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9EXY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLVYGDILI----DSKDHGIIERKYPDRLNYFYWSIKSLCHQATFIRKNLFDLYGYYNEEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKISIITINLNNLEGLRKTLESVKSQTYTNFELIVVDGGSTDGSFEYLKSNLDLIKKFIS
                                                                                                            SGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLYYGDVVM
                                                                                                                                                            SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV-VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLVYGDVVMRSTKSRHAGPFDL----DRLLF----ETNLCHQSIFYRRELFDGIGPYNLRY
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VRVLKRDDIKVSYVPQV
                        IRCFSNPALITRYMDVV
                                                                       RS-----TKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFN
                                                                                               SESDKGIYDALNKGINLSTGDIIGFVHSDDVLARPDIIETIVGRFHETKAD-VVYGDLVF
                                                                                                                                              SIITVTYNSEKTLRNTLESIELQTYSDIEYIIIDGGSTDNTLKIIN----EVSTRVTRCL 59
                                                FEKNQIDIIKRYWRSGPFKRSKLSLGWAPPHPSFYMRRELYKDDGYFDLSYRIAADYDQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                             1 Similarity
67; Conserv
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                                                                                                                                                                                                                                            248 AA;
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                                                                                                                                                                                                                                              28560 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Enterobacteriaceae;
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Last annotation updat
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                                                                                                                                                                                                         Score 266.5;
Pred. No. 2.
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RESULT 13 Q9ZGK3

Q9ZGK3

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RESULT
Q9EXZ1
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Best Local S
Matches 67
Query Match
Best Local S
Matches 74
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01-MAR-2001 (TrEMBLrel. 16, Cree
01-MAR-2001 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Putative glycosyl transferase.
Salmonella enterica subsp. ente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalambaheti T., Bulach D.M., Rajakumar K., Adler B., "Genetic organization of the lipopolysaccharide O-an locus of Leptospira borgpetersenii serovar Hardjobov Microb. Pathog. 27:105-117(1999).
EMBL; AF078135; AAD12966.1; -
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00335; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leptospira borgpetersenii.
Bacteria; Spirochaetales; Leptospiraceae;
NCBL_TaxID=174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 29.0 kbm protein.
                                                                      InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                in Salmonella enterica.";
Microbiology 147:599-610(2001).
EMBL; AY012186; AAG41745.1; -.
                                                                                                                                                                                                                                                                                                                               Q9EXZ1
                                                              Transferase
                                                                                                                                                                            STRAIN-M264;
                                                                                                                                                                                                                             Salmonella.
                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09ZGK3;
                                                                                                                                                               MEDLINE-21135136; PubMed-11238967;
                                                                                                                                                                                                               NCBI_TaxID=59201;
                                                                                                                                                                                                                                                                                                                                                                                            179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                  Jensen S.O., Reeves P.R.
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                       Molecular evolution of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MLIESKEGNLRLGROPPVMTLSHLLLDT-IMHPACLIKRKLFERYGLYDLNFRIVADYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVMRSTK----SRHAGPEDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDF::: | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVFSIIIPTFNAAVTLQACLGSIVGQ-TYREVEVVLVDGGSTDRTLDIANSFRPELGSRL
                                                                                                                                                                                                                                                                                                                                                                                                                 NIRCESNPALITRYMDVVISEYNDMTGESMRQGTD----KEERKRLPMYF
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67; Conserv
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 n 18.2%;
Similarity 28.1%;
74; Conservative 5
                                                 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                 ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.2%;
29.1%;
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                                                  29275
                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
Score 255; DB
Pred. No. 2.2e
52; Mismatches
  52;
                                                                                                                                                                                                                                                     enterica.
                                                                                                                                       GDP-mannose
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 255.5; DB Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                              PRT;
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                                                 39759CD9576DB137
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 es 89;
                                                                                                                                       pathway
                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hardjobovis
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                                                                                                                                                                                                                                        Enterobacteriaceae;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE-99403407; PubMed-10474199; de la Pena-Moctezuma A., Bulach D.M., Kalambaheti T., Adler B.; de la Pena-Moctezuma A., Bulach D.M., Kalambaheti T., Adler B.; "Comparative analysis of the Use biosynthetic loci of the genetic subtypes of serovar Hardjo: Leptospira interrogans subtype Hardjoprajitno and Leptospira borgpetersenii subtype Hardjobovis."; FEMS Microbiol. Lett. 177:319-326(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De la Pena-Moctezuma A., Bulach D.M., Submitted (APR-1999) to the EMBL/GenB EMBL; AF144879; AAD52183.1; -. InterPro; IPR001173; Glycos_transf_2. Pfam; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 2
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01-MAY-2000 (TrEMBLrel. 13, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Hypothetical 30.4 kDa protein.
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                    VVMRSTK----
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                                                       NIRCESNPALITRYMDVVISEYNDMTGESMRQGTD----KEERKRLPMYF
                                                                                                                                                                                                                                                                                 VVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGD 122
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                                                                                                                                                                                                                               ---SEPDLGIYYGQNKGILNSKGEYILFLNSGDTLASENTLTDILSF---ELSSDLIYGD
                                                                                                            MLIESKEGNLRLGRQPPMMTLSHLLLDT-IWHPACLIKRKLFERYGLYNLNFRIAADYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
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263 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                            -SRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30417 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bulach D.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lach D.M., Kalambaheti T., A
EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 254.5; DB 2
Pred. No. 2.6e-14;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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J. Bact
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                                                                              SEQUENCE OF 1-131 FROM MEDLINE=90264305; Pubme
                                                                                                                    cyanobacterium Anabaena sp
DNA Res. 8:205-213(2001).
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                                                         Holland D., Wolk C.P.; "Identification and characterization
                                                                                                                                         Yasuda M., Tabata S.;
"Complete genomic sequence
                                                                                                                                                                 Nakazaki N., Shimpo
                                                                                                                                                                            Watanabe A., Iriguchi M., Ishikav
Kishida Y., Kohara M., Matsumoto
                                                                                                                                                                                                                                                NCBI_TaxID=103690;
                                                                                                                                                                                                                                                             Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
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                                                                                                                                                              PubMed=11759840;
rra Y., Wolk C.P., Kuritz T., Sasamoto S.,
ruchi M., Ishikawa A., Kawashima K., Kimura T.
ra M., Matsumoto M., Matsuno A., Muraki A.,
po S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                 FROM N.A.
PubMed=2111805;
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36; Mismatches
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STRAIN=K12 / MG1655;
STRAIN=H12 / MG1655;

K MEDLINE=94316500; PubMed=8041620;
K MEDLINE=94316500; Punded V., Daniels D.L., Plunket RT "Analysis of the Escherichia coli genome. V. region from 76.0 to 81.5 minutes.";
region from 76.0 to 81.5 minutes.";
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EMBL; AF031959; AAC32401.1; ALT_INIT.
PIR; B35391; B35391.
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                MEDLINE-89174812; PubMed-2647748; Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.; "The primary structure of Escherichia coli L-threonine
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                            Putative glycosyl YIBD OR B3615.
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01-JUL-1989 (Rel. 11,
01-OCT-1994 (Rel. 30,
16-OCT-2001 (Rel. 40,
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                                                                                   3101. Chem. 264:5226-5232(1989).
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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Q57022; P96336;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUN-2002 (Rel. 4
EMBL; U32768; HSSP; P39621; TIGR; HI0868;
                                                                                                                                                                                                 Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
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SEQUENCE
                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                      Science 269:496-512(1995).
Science 269:496-512(1995).
STATIARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; P
Haemophilus
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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PIR; B33276; B33276
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MEDLINE-95350630; PubMed-7542800;
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                                                                                                 the European
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MEDLINE=9535630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness I Relischmann R.D., Adams M.D., White O., Clayton R.A., Merrick i Rerlavage A. R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick i Rerlavage A. R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Catu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                           Hypothetical protein;
                                                                          EMBL; U32832; AAC23227.1; TIGR; HI1578; -.
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15-JUN-2002 (Rel.
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7CBC2681039AB5B4 CRC64;

EMBL; U38473; AAC77840.1; EMBL; AE000295; AAC75116.1 EcoGene; EG13573; wcaE.

AE000295; AAC75116.1; ne; EG13573; wcaE.

Glycos_transf_2.

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Best Local
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MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
Gregor J., Davis N.W., Kirkpatrick H.A., Goe
                                                      the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                    This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                          STRAIN-K12;
Reeves P.R.;
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16-OCT-2001 (Rel. 40, Last ann
Putative colanic acid biosynth
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96326333; PubMed=8759852;
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Science 277:1453-1474(1997).
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Interpro; iPR001173; Glycos_transf_2.
Pfam; PF00534; Glycos_transf_1; 1.
Pfam; PF00535; Glycos_transf_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multicellular development.";
J. Bacteriol. 178:1631-1639(1996),
-!- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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01-NOV-1997
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                                                                                                         Lipopolysaccharide biosynthesis.
SEQUENCE 1275 AA; 139596 MW;
                                                                                                                                                                                                                                                                        EMBL; U36795; AAB05019.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96198166; PubMed=8626291;
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation updat
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pfam; PF00535; Glycos transf.2; 1.
Exopolysaccharide synthesis; Transferase; Glycos
exopolysaccharide synthesis; Transferase; Glycos
exopolysaccharide 301 AA; 34788 MW; 99D0EE3080E6EC06
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MOI. Microbiol: 15:917-933(1995).

FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF AMYLOVORAN WHICH FUNCTION: AS A CLYCOSYI FROM THE STROME FROM UDP-GALACTOSE TO TRANSFERASE WHICH TRANSFERS GALACTOSE FROM UDP-GALACTOSE TO LIPID-LINKED AMYLOVORAN-SUBUNIT PRECURSOR.

LIPID-LINKED AMYLOVORAN-SUBUNIT PRECURSOR.
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InterPro; IPR001173; Glycos_transf_2.
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                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed
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MEDLINE=95350630; PubMed=7542800;
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EMBL; U32842; AAC23342.1;
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RX KUISTE-98044033; PubMed-9384377;
RX KUISTE-98044033; PubMed-9384377;
RX KUISTE, Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Horizs R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Decizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Guiseppi S., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Jauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey.M., Reynolds S.,
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Hullo M.F., Ionescu M., Lubochinsky B., Marceli
Presecan E., Santana M., Schneider E., Schweize
Rapoport G., Danchin A.;
"Bacillus subtilis genome project: cloning and
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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Sekiguchi J., Sekowska A., Seror S.J., Serror P., Soffone F.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamanoto H., Tamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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EMBL; Z99123; CAB15824.1; -.
PIR; S39711; S39711.
Subtilist; BC10602; ywdF.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
Complete proteome.
Complete Proteome.
SEQUENCE 268 AA; 30616 MW; DD8428F7016EC9B3 CRC64;
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

DNA Res. 3:137-155(1996).

Integral membrane protein (Potential).

SIMILARITY: TO Y. PESTIS HMS LOCUS PROTEIN HMSR AND TO S.EPIDERMIDIS ICAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miti T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See )
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PF00535; Glycos_transf_2; 1.
hetical protein; Transmembrane;
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D90739; BAA35803.1; -.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
succinoglycan biosynthesis protein exoU (EC 2
EXOU OR RB1071 OR SMB20948.
                                                                                                                                                                                                                                                                                                      EMBL; L20758; AAA16053.1; -. EMBL; Z22646; CAA80359.1; -. EMBL; AL603645; CAC49471.1; PIR; D49348; D49348.
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MEDLINE-94162682; PubMed-8118055;
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                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Bioinformat
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J. Bacteriol. 175:7033-7044(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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Pfam; PF00535; Glycos_transf_2; 1.
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fixing endosymbiont Sinorhizobium mellioti.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

-I- FUNCTION: GLYCOSYLTRANSFERASE REQUIRED FOR THE SYNTHESIS OF

SUCCINGLYCAN (EPS I). NEEDED FOR THE ADDITION OF THE FIFTH SUGAR

(GLUCOSE). CATALYZES THE FORMATION OF A BETA-1,6 LINKAGE BETWEEN

THE FOURTH AND FIFTH SUGAR.

-I- PATHWAY: Exopolysaccharide biosynthesis.

-I- SUBCELULIAR LOCATION: Cytoplasmic.

-I- SUBCELULIAR LOCATION: Cytoplasmic.

-I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification and analysis of the Rhizobium meliloti exoA involved in exopolysaccharide biosynthesis and mapping of pocated on the exoHKLAMONP fragment.";
Mol. Gen. Genet. 241:367-379(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21396508; PubMed-11481431; Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gour Golding B., Puehler A., "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The complete sequence of the 1,683-kb psymB megaplasmid from "The c
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Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision;
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MEDLINE=94067019; PubMed-8246891;
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15-JUN-2002 (Rel. 41, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
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                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                 CAUTION: Ref.1 sequence differs from frameshift in position 208.
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Best Local S
Matches 69
                                                                        J. Bacteriol. 183:3564-357042001.
-!- PATHWAY: Lipopolysaccharide core biosynthesis.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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Pfam; PP00535; Glycos_transf_2; 1.

Transferase; Glycosyltransferase; Exopolysaccharide synthesis;
Plasmid; Complete proteome.
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EMBL; Z22636; CAA80347.1; -.
EMBL; AL603645; CAC49484.1; -.
                                                                                                                       "Genetic characterization of the Klebsiella pneumoniae waa gene cluster, involved in core lipopolysaccharide biosynthesis.";
J. Bacteriol. 183:3564-3573(2001).
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30-MAY-2000 (Rel.
                  the European Bioinformatics Institute.
                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ED
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PIR; S37029; S37029.
PIR; S39958; S39958.
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                                                                                                                                                               Regue M., Climent N., Abitiu N.,
Altarriba M., Tomas J.M.;
                                                                                                                                                                     STRAIN-C3;
MEDLINE-21264367; PubMed-11371519;
MEDLINE-21264367; PubMed-11371519;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Klebsiella.
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                                                                                                                                                                                                                                                                                                                               39, Created)
39, Last sequence update)
41, Last annotation update)
e core biosynthesis glycosyl
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           institutions as long
                                                                                                                                                                                                                                                                              gamma subdivision; Enterobacteriaceae;
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Pred. No. 6.1e-05;
7; Mismatches 129;
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                        restrictions
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                                                  a collaboration
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                        InterPro; IPR001173; Glycos_transf_2.

Pfam; PF00535; Glycos_transf_2; 1.

Lipopolysaccharide biosynthesis; Transferase; Gl
SEQUENCE 258 AA; 29268 MW; D7458899030678D9
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               EMBL; AF146532; AAD37772.1;
154 LG 155
                         162
                                                      109 SIARRNYFLGRFMRHSGWYPDRVLRL-----
                                                                               102 TLAQVAAFLGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDG 161
                                                                                                            58
                                                                                                                                     67
                                                                                                                                                                  6
                                                                                                                                                                                     7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
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                                                                                                                                       GPDDGPYDAMNRGVGV-----ATGEWVLFLGADD-----
                                                                                                                                                               SVYMIAKNAADLLPDCLGSV---SWAD-EIIVLDSGSTDNTVELAR----RLGAQVYTHT
                         IG 163
                                                                                                                                                                                                                      Conservative
                                                                                                            9.4%;
                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                     Score 131.5;
Pred. No. 7.1e
32; Mismatches
                                                      -YERARYRYNDNLVHESL---
                                                                                                                                                                                                                                 5; DB 1;
7.1e-05;
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                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                     Gaps
                                                                                                            108
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9;

Search completed: April Job time : 24 secs 17, 2003, 17:27:24

174.5 12.5 996 173.5 12.4 324 173.5 12.4 338	177.5 12.7 343 2 175 12.5 318 2 174.5 12.5 333 2 174.5 12.5 623 2	188.5 13.5 333 188 13.4 299 182 13.0 344 178 12.7 356	190.5 13.6 323 2 190 13.6 248 2 190 13.6 248 2 190 13.5 248 2 189.5 13.5 333 2	14.0 337 2 14.0 367 2 13.7 336 2 13.6 322 2	205.5 14.7 298 2 204.5 14.6 330 2 202.5 14.5 262 2	220 15.7 324 2 207 14:8 321 2 206.5 14.7 316 2	232.5 16.6 260 2 231.5 16.5 259 2	56.2 275 17.0 247	No. Score Match Length DB ID		 Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d 	3: pir3:* 4: pir4:*	PI	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Total number of hits satisfying chosen parameters:	earched: 283224 seqs, 96134422 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-09-705-911-24 Perfect score: 1401 Sequence: 1 MTAPVFSIIIPTFNAAVTLQALRTRI	Run on: April 17, 2003, 17:25:05; Search time (without a. 544.080 Mi	OM protein – protein search, using sw model	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
o o rei	glucosyltransferas hypothetical prote sugar transferase	glycosyltransferas probable glycosyl probable glycosylt hypothefical profe	hypothetical prote probable glycosyl glycosyl transfera hypothetical prote	တ္ဆ		hypothetical prote hypothetical prote hypothetical prote	hypothetical prote conserved hypothet	hypothetical prote . probable glycosylt	Description		by chance to have a ne result being printed, distribution.					283224			ALRTRLIRVKAVSKERSAEP 266	Search time 47 Seconds (without alignments) 544.080 Million cell updates/sec	•	4578 Ltd.
QY 181 CESNPALITRYMDVVISBYNDMTGFSMRQGTDKEEFKKRLPMYFWVAGWETCRRMLAFLKD	Qy 121 GDVVMRSTKSRHAGPFDLDRLLFETNLCHOSIFYRRELFDGIGPYNLRYRVWADWDFNIR : : : :	Oy 61 RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120 ::	Qy 1 MTAPVESIIIPTFNAAVTLQACLGSIVGOTYREVEVVLVDGGSTDRTLDIANSFRPELGS 60 :	Query Match 56.2%; Score 788; DB 2; Best Local Similarity 60.9%; Pred. No. 2.6e-64; Matches 156; Conservative 24; Mismatches 54	** ** *	Residues: Cross-ref Genetics:	A;Accesson: 57004 A;Status: preliminary A;Molecule type: DNA		Smith, D.R.; Robison, K. bmitted to the EMBL Data Lil	A;Cross references: GB:Z83018; GB:AL123456; NID:g3261671; A;Experimental source: strain H37Rv	Accession: B70570 Accession: B	A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S. A;Title: Deciphering the biology of Mycobacterium tuberculosis A;Reference number: \$70500. MITD. 8828587. burn. 0524230	R;COle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T. Rajandream, W.A.; Rogers, J.; Rutter, S.; Seeger, Nature 103 537-544 1000	nat es: 17 sio	B70670 hypotheti		ALIGNMENTS	11.7 334 1	168 12.0 1013 2 165.5 11.8 340 2 165 11.8 303 2	12.0	170.5 12.2 301 2 170 12.1 354 2	173.5 12.4 338 172.5 12.3 344 172 12.3 573 171 12.2 344
MYFWVAGWETCRRMLAFLKD 240 	GIGPYNLRYRYWADWDFNIR 180 TIGPYNLRYRVLADWDFNIR 199	TTLAQVAAFLGDHAASHLVY 120 : : DTLARVAAFIGEHEPSDLVY 139	AGGSTDRTLDIANSFRPELGS 60 	2; Length 275; 54; Indels 22; Gaps 2;	ınsferase A	N:AAA50938.1; PID:g560517		Ebc2.		3261671; PIDN:CAB05419.1; PID:g1694	shown; translation not shown	Whitehead, S.; Barrell, B.G. tuberculosis from the complete gen-	f.; Churcher, C.; Harris, D.; Gordo ; Gentles, S.; Hamlin, N.; Holroyd K.; Skelton, S.; Squares, S.	#text_change 20-Jun-2000	oulosis (strain H37RV)			glycosyl transfera hypothetical prote	yalacusamine cunt hypothetical prote glycosyl transfera glycosyltransferas	nypornetical prote probable glycosyl glycosyl transfera hypothetical prote		probable regulator hypothetical 40.5k hypothetical prote capsular polysacch

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Species: Helicobacter pylori
; Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: E71975
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71975
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E71975
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AG0376
      ş
                                                                                                                                                                                 A;Cross-references: GB:AE001448; GB:AE001439; NID:g4154594; PIDN:AAD05675.1; PID:g41546(A;Experimental source: strain J99
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-260 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein jhp0094 - Helicobacter pylori (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA :Residues: 1-247 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Yersinia
C; Date: 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable glycosyltransferase wbyL [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: AB0001; A; Accession: AG0376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: AG0376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:AL590842; PIDN:CAC92338.1; PID:g15981048;
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
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                                                                      Local
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                                                                                                                                      jhp0094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------VMRSTKSRHAGPEDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWAD 174
    SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ES--DQGIYDALNKGIDLATGDIIGFLHSDDLLAYPGALSDIVETF-EKQQCDAVYGDLQ
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                                                                      Similarity
                                                  Conservative
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                                                                    16.6%;
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                                                                      Score
Pred.
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Pred. No. 3.3e-14;
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                                                  Mismatches
                                                                    232.5;
No. 1.
                                                      υВ 2;
1.2e-13;
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                                             39;
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                                             Gaps
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                                                                                                                                                                                                    RESULT 5
AB2190
Nakazaki, N.; Shimpo, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
                                                         C; Accession: AB2190
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                      C: Species: Nostoc sp.
                                                                                                                                                                             hypothetical protein alr3073 [imported] - Nostoc sp. (strain PCC 7120)
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66

S.; Sugimoto,

X :

Kuritz, T.; ; Takazawa, 1 Filamentous

Sasamoto, S.;

Watanabe, Yasuda,

7120

Nitrogen-fixing Yamada,

Cyanobacterium

Sequence of the

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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, F. Peterson, S.; Loftus, B.; Rlchardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; MCK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujli, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997

A;Autthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
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A; Residues: 1-259 < TOM>
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C;Date: 09-Aug-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: F64532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein HP0102 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: F64532
                                                                                                                                                                                                                                                                                                                               Matches
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                                        180
181
                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                            62 EKDEGIYDAMNKGIKRSSGDIIALLNSDD-FYKDEFVVEKVVHEFERKNCDSVYADLVFV
                                                                                                                                                                                                  67 GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVM- 125
                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                    7 SIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSERPELGSRLVVHS
                                                                               KPDCLEKVVRYYEIGEFNPKTLLYGVVPAHPTLFVKKAIYERYGLYKTDYKISADFEMII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKDKENRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPDCLEKVVRYYESGEFSPKTLLYGVVPAHPTLFVKKAIYERYGLYKTDYKISADFEMII 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLFVVQKISFSYLKEVL 197
                                    RCFSNPALITRYMDVVI 196
                                                                                                                                                                                                                                           SVITACENSEKTIEDTILSVLHQTYKNIEYIIIDGASTDSTLEIIQKHRDKIA---CVMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCFSNPALITRYMDVVISEYNDMTGFSMRQG--TDKEFRKRLPMYFWVAGWETCRRMLAF
                                                                                                                     -----RSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNI 179
                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AE000532; GB:AE000511; NID:g2313184;
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                                                                                                                                                                                                                                                                                                                                                Score 231.5; DB 2
Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                             Mismatches
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76.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
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A; Gene: alr3073
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                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: AB2190
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-321 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein alr3062 [imported] - Nostoc sp. (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG2188
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                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 MLAFLKDKENRRLALRTRLIRVKAVS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 DWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 VMRSTKSRHAGPFD-----LDRLL--FETNLCHQSIFYRRELFDGIGPYNLRYRWA 173
                                           118 AYIDEQGKSTGKIFKNQVEGYVWPQLTEHNIVECGSVALVRRVCFEKMGLFDRNLGSYV- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                        59
                                                                                                                                                         64 VHSGPDDGPYDAMNRGVGVATGEWYLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV 123
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                                                                                                                                                                                                                                                                          4 PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTIDDKGELLKPFEPLYEGNVYTDLLLANFLTNGSNPLI--RKAAIASIGEFDTTLRSGE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKISVIIPAYNAERTILETINSVLNQTFSDLEIIVINDGSTDRTVEVLQNVD----DARLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWDYWLR-----LAYKWPFVVVKQHQIL---YRRSVTSKSFKLQI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYSYENSRASGARNHGISHAVGDFISFLDADD-LWTPDKLELQLSALNNHPEAGVAYSWT 117
                                                                                      VMRSTKSRHAGPFDLDRL------LFETNL--CHQSIFYRRELFDGIGPY--NLRYRVW 172
                                                                                                                                    LISOANOGLAGARNTGIVNASGEYIAFLDADD-IWEPTKLAKQVSVLDENPTVGLVYTWV
                                                                                                                                                                                                                               PKVSVVIPAYNAMPYLPETLESVLRQTYHDFEVVVVNDGSSDNTEEWVSQI---LDPRLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASLAILDKAMKVLPLELQYLKKHSLS 241
ADWDENIRCESNPALITRYMDVVISE
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                                                                                                                                                                                                                                                                                                                                             14.8%; Score 207; DB 2; Length 321; 32.0%; Pred. No. 3.4e-11;
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Pred. No. 2.3e-12;
                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 324
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A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 30-Jun-2002 C;Accession: AE2189

R;KaneKo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosyl transferase PAB0772 - Pyrococcus abyssi (s
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
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A;Residues: 1-316 <KUR>
A;Residues: 1-316 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74767.1; PID:g17132162; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: Ab1807; MUID:21595285; PMID:11759840
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                                                                                                                                                                                      C; Superfamily: Neisseria meningitidis glycosyl transferase
                                                                                                                                                                                                                                                            A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-298 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
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                                                                                                Matches
                                                                                                                                      Query Match
                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                               Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50071.1; PID:g54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 VMRSTKSRHAGP-----FDLD---RLLFETNLCHQS-IFYRRELFDGIGPYNLRYRWAD
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nes 55; Conserv
                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDV
                                                                                                                                                                                                                PAB0772
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                                           1 MTAPVESIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSERPELGS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFMDEQGKSSIPGVSLFFEGDVQAHLLVNNFLASGSNPLIRKQAIESVGEFDSNCMGCAD
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MSRPIVSVIIPTYNRANLLRRAIASVLNQKFKDFELIVVDDASTDNTPEVVESI--EDGR
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                                                                                                                                                                                                                                                                                                                                                                                                                     abyssi genome sequence: insights into
                                                                                                                   14.7%; Score 205.5; DB 2 29.0%; Pred. No. 4.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus abyssi (strain Orsay)
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                                                                                             Mismatches
                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 20-Jun-2000
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                                                                                                                                           298;
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hypothetical protein Rv1514c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Bate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: E70714
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holro, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete (A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8, 205-213, 2001

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An:

A: Reference number: AB1807; MUID: 21595285; PMID: 11759840
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazav
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A; Residues: 1-330 < KUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204.5; DB Pred. No. 6e-11; 8; Mismatches 8
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                                                                                                       Holroyd,
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                                                                                                                          Gordon,
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A; Experimental source: strain F
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A; Residues: 1-262 <COL>
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A; Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-337 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number:
A; Accession: AG1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary;
AAQDRDFFLSVVMNGAKVAYQPGCYAVYRRYGSVTVS
                                VWADWDFNIRCFSNPALIT --
                                                                                                                              YPQQGGNHARNRGFELSQGEYIQYLDADDYIL-PEKIEKQVNFL-ETTGADVVYGD----
                                                                                                                                                           GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVMR 126
                                                                                                                                                                                             SVIIPCFNAEKWIREAIESCLTQTYADVEIIVIDDGSTDNSLEIIKTF----GNEIIWRS
                                                                                                                                                                                                                            SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQ-VAAFLGDHAASHLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPTVSVITISFNDLDGLQRTVKSVRAQRYRGRIEHIVIDGGSGDDVVAYLSGCEPGFA-
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                                                             WRHQRHL-PDDSSFLDKIEISGVQADILAALLANWWVALAALMYKRSVVENSDRWDETLP 182
                                                                                             STKSRHAGPFD---LDR-----
                                                                                                                                                                                                                                                              61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimpo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain PCC 7120 is a synonym of Anabaena sp.
1 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                           enomic Sequence of the Filamentous Nitrogen-fixing AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALVCEPVTIRCVLCEF-DTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wighter T.; Sasamoto, M.; Takazawa, M.; Yamada, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%;
                                                                                                                                                                                                                                                                            14.0%; Score 196.5; DB: 28.1%; Pred. No. 3.3e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; GB:AL123456;
H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                              Mismatches
                                                                                            ----LLFETNLCHQSIFYRRELFDGIGPYNLRYR 170
                                -RYMDVVIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nostoc sp. (strain PCC 7120)
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219
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                                                                                                                                                                                                                                                                                           337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain PCC
30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                               GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe,
; Yasuda, 1
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RESULT -\97168
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G95948
A;Caterno.
                                                                                                                                                                                                                                                                                                                                                                                   R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, Capol
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lycosyltransferase [imported] - Clostridium acetobutylicum
;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: A97168
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain 1021, megaplasmid pSymB R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hübler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

'cience 293, 668-672, 2001
'Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A; Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-336 <KUR>
A; Cross-references: GB.AE001437; PIDN: AAK80132.1;
A; Experimental source: Clostridium acetobutylicum
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     S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPTPVVSIVLPVYNAEPYIAAAIESVLRQDYERLEVIAIDDGSTDRSRDILERYR-KSDS
PKVSIVMPVYNSERYLAEAIESILDQTYNDFEFIIVDDGSTDESYNIISSYANK-DNRII
                       PVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVSIISRENRGLIATLNEGLALAKGELIARMDADDIAYPSRLSRQVALFSAEPRLALSGT
                                                                                                       Similarity
65; Conser
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Pred. No. 3.7e-10;
33; Mismatches 78;
                                                                                                    Score 192; DB 2; 1
Pred. No. 8.5e-10;
57; Mismatches 113;
                                                                                                                                                                                                                                                              PID:g15025168;
ATCC824
                                                                                                                                                    Length
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C; Accession: AD2189
R; Kaneko, T.; Nakamura,
Nakazaki, N.; Shimpo, S
DNA Res. 8, 205-213, 200

S.; Sugimoto, M.; Takazawa, I

X :.

Sasamoto,

S.; V

Watanabe, ; Yasuda,

A .

; Irig Tabat

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Cyanobacterium

A; Accession: AD2189 A; Status: prelimina

A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Reference number: AB1807; MUID: 21595285; PMID: 11759840

A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001

Anabaena sp. #text_change

strain 30-Jun-

PCC --2002

hypothetical protein alr3067 [imported] - Nostoc sp. (strain PCC C; Species: Nostoc sp.

RESULT AD2189

15

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A; Cross-references: GB:BA000019; PIDN:BAB74535.1; A; Experimental source: strain PCC 7120
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A; Residues: 1-322 < KUR>
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2160
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C.Species: Nostoc sp.
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Nakazaki, N.; Shimpo, S
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 183
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                                                              GNDKTIDQASTQGPKLSEDLASVILQTGNAWCFPPTSGLAYRREVLEKVFPIDPVKWRIW
                                                                                            RSTK----SRHAGP----FDLDRLLFETN--LCH---QSIFYRRELFDGIGPYN-LRYRVW
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29.1%; Pred. No. 1.
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; Takazawa, M.; Yamada, M.; Yasuda,
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A; Residues: 1-323 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74766.1; PID:g17132161; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
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                                                        165 LIRRAAIDSVGLEDPTLKSCEDWDEYLRLAAKWQEALVKKAQIIYRQSPTAWTSKLDVM 223
                                                                                                   128 YKFANEADSYADESNSFAGD------VYAELLIKNFLQNGSNP------ 164
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

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ALIGNMENTS

RESULT 1 AAW21774

AAW21774 standard; Protein; 266 AA.

XXXX AAW21774;

11-MAR-1998 (first entry)

XX EX P

Protein encoded by ORF F of GS region in M. avium subspecies silvaticum.

GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease.

Mycobacterium avium subspecies silvaticum.

X SO X WO9723624-A2

XXXX 03-JUL-1997.

23-DEC-1996; 96WO-GB03221.

PA DR XX PA 21-DEC-1995; 95GB-0026178.

(SGEO-) ST GEORGE'S HOSPITAL MEDICAL SCHOOL.

Doran T, Ford J, Sumar N, Tizard M; Hermon-Taylor J, Loughlin M, Millar D;

WPI; 1997-351061/32. N-PSDB; AAT74469.

New isolated pathogenicity island from mycobacteria used ç

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RESULT 2
AAW21775
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Best Local
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                                                                                                                                                                                          GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease. vaccine; inflammatory disease; sarcoidosis; Johne's disease.
                                                                                                                                                               Mycobacterium
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                                                                                                                                                                                                                                                           Protein encoded by ORF F of the GS region in M. paratuberculosis
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                                21-DEC-1995;
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hes 266; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRRMLAFLKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                               paratuberculosis
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                              95GB-0026178.
                                                               96WO-GB03221
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Pred. No. 7.3e-144;
); Mismatches 0;
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                                                                                                                                                                                                             disease;
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Sequence

266 AA;

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The present sequence represents a protein encoded by open reading frame (ORF) F of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity. Such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies and the intestine and Crohn's disease in humans. The protein products of the intestine and Crohn's disease in humans. The protein products of the intestine and Crohn's disease in particular they can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohn's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran
Sumar
                                         sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 51; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       of mycobacteria infections
                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated pathogenicity island from mycobacteria - develop products for detection, diagnosis, prevention
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DB; AAT74470.
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Tizard |
                                     in humans or Johne's disease in animals.
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밁 Ş 밁 Q 망 Š Ş . **В** QY Query Match Best Local Sin Matches 266; 241 181 181 121 121 61 61 _ I MTAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS CFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRRMLAFLKD GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR 180 KENRRLALRTRLIRVKAVSKERSAEP RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120 MTAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY Similarity Conservative 100.0%; 0, Score 1401; DB 18; Pred. No. 7.3e-144; Mismatches 266 0; 0; Gaps 120 240 60 60 240

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AAW21783
      RESULT 3
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241

266

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AAW21783 standard;
Protein;
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AAW21783;

11-MAR-1998 (first entry)

Protein encoded by ORF F from the GS region of M. tuberculosis

GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss. Mycobacterium

W09723624-A2

(SGEO-)

ST GEORGE'S

HOSPITAL MEDICAL

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RESULT 4
AAW88309
ID AAW8
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AC AAW8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the protein encoded by open reading frame (ORR) F, from M. tuberculosis. This ORF F has been found to have homoogy with ORF F of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of 8 kb of DNA comprising a core region of 5.75 kb. The CW with multiple ORFs and an adjacent transmissable element of 2.5 kb. The CORFs, and also the transmissable element, encode proteins which may be controlled in the controlled proteins which may be consistent to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies silvaticum. These pathogenic mycobacteria cause chronic inflammation of the intestine and Crohn's disease in humans. The protein products of the intestine and Crohn's disease. In particular they can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can be used as vaccines for inflammatory diseases such as Crohn's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Sumar N,
                                                                                                                                                          AAW88309 standard;
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                                26-APR-1999
                                                                                               AAW88309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDVVMRSTKSRHAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFNIR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRLPMYFWVAGWETCRRMLAFLKD
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Tizard M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 AA;
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                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-GB03221
                                                                                                                                                          Protein;
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60.9%;
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Pred. No. 4e-77;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O antigen; Olll antigen; wbdL gene; colitose transferase; glucose transferase; diarrhoea; haemorrhagic colitis; diagnosis.
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N-PSDB; AAX06748.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1997;
01-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli strains that cause diarrhoea and haemorrhagic colitis
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                                 212 DKEFRKRLPMYFWVAGWETCRRMLAFLKDKENRRLALRTRLI 253
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                                                                                                                                                                                                                                                                                    15 LDAPLVSIIIATYNSELDIAKCLQSVTNQSYKNIEIIIMDGGSSDKTLDIAKSFKDD---
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   TLE-
                                                                                                                                                                            GDVVMRSTKSRHAGP------FDLDRLLFETNLCHQSI-----FYRREL
                                                                                                                                                                                                                                                  RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                                                                                       FDGIGPYNLRYRVWADWDFNIRCF-----SNPALITRYMDVVISEYNDM-TGFSMRQGT 211
                                                                                                                                           G-----RTAHEGPDRNISGFSGSEWYNLTGFKFNYYKCNLPLPIMSAIYSRDFFRNER
                                                                                                                                                                                                               RIKIVSEKDRGIYDAWNKAVDLSIGDWVAFIGSDDVYYHTDAIASLMKGVMVSNGAPVVY
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                                                                      ---IKLKIVADADWFLRCFIKWSKEKSPYFINDTTPIVRMGYGGVSTDISSQVKT
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97AU-0006545
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-----SFIVRKKNNISCLNIQLI
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RESULT 5
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Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the genomic sequence of pyrococcus abyssi (see AAF86431 and AAH4123-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Pages 981-982; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forterre P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1999;
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                                                                                                                                                                                                                                      1 MTAPVESIIIPTENAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGS 60
                                                                                                         GVVYGGFYYVSQDGRILGKRLPKHRGDI-YSHLLKENFIGSPTLLIRRECFKKAGLFDPR
                                                                                                                                    HLVYGDVVMRSTKSR-------HAGPFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLR 168
                                                                                                                                                                                         ----RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAAS 116
                                                                                                                                                                                                                   HLDIW 231
                         RLPMY 222
                                                  LSSSQDWDMWLR-----IARYYKFDYVDEIIAKYYVHGKQISFNMKKYIPGRERLIRK 226
                                                                             YRVWADWDFNIRCFSNPALITR----YMDVVISEY---NDMTGFSMRQ---GTDKEFRK 217
                                                                                                                                                              IRYIRLKKNSG----GPI-ARNIGIKKAKGRFIALLDDDDEWLPHRLEVQVRKFENLGKEF 114
                                                                                                                                                                                                                                                                                                                                 298 AA;
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                                                                                                                                                                                                                                                                                       14.7%; Score 205.5; DB 2
29.0%; Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                                            38;
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Saurin W, Heilig R;
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                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                            99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lecompte
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encode
                                                                                                                                                                                                                                                                                                      298;
                                                                                                                                                                                                                                                                          37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. abyssi is
                                                                                                                                                                                                                                                                          Gaps:
                                                                                                         173
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Doran T,
Sumar N,
                                                                                                                                                                                                           WO9723624-A2
                                                                                                                                                                                                                                                                                   GS; pathogenecity island; pathogenic protein; mycobacterial disease; cellular recognition receptor; pathogenic mycobacteria; Crohn's disease; vaccine; inflammatory disease; sarcoidosis; Johne's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW21779;
                                                                                                                                  23-DEC-1996;
                                                                                                                                                                       03-JUL-1997
                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                             Protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1998
                                                        (SGEO-) ST GEORGE'S HOSPITAL MEDICAL SCHOOL.
                                                                                               21-DEC-1995;
                   Ford J,
 Tizard M;
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                  tuberculosis.
                                                                                             95GB-0026178
                                                                                                                                  96WO-GB03221
                   Hermon-Taylor J,
                                                                                                                                                                                                                                                                                                                                                             ORF B from
                                                                                                                                                                                                                                                                                                                                                             the GS
                   Loughlin M,
                                                                                                                                                                                                                                                                                                                                                             region of M.
                                                                                                                                                                                                                                                                                                                                                             tuberculosis
                     Millar
                     D,
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New isolated pathogenicity island from mycobacteria - develop products for detection, diagnosis, prevention of mycobacteria infections used and t ç

WPI; 1997-351061/32 N-PSDB; AAT74473.

Claim 1; Page 53; 62pp; English.

The present sequence represents the protein encoded by open reading frame CC (ORF) B, from M. tuberculosis. This ORF B has been found to have homogy CC with ORF B of a novel polynucleotide sequence designated "CS". GS is a comparison of a novel polynucleotide sequence designated "CS". GS is a comparison of 2.5 kb. The CC with multiple ORFs and an adjacent transmissable element of 2.5 kb. The CC with multiple ORFs and an adjacent transmissable element, encode proteins which may be comparison. GS was discovered and characterised using differential DNA CC analysis technology. It is found within Mycobacterium paratuberculosis and it has also been identified in Mycobacterium avium subspecies CC silvaticum. These pathogenic mycobacterium avium subspecies comparison of the intestine and Crohn's disease in humans. The protein products of the CC care of GS can be used for detecting mycobacteria or for diagnosing, comparison of the cused as vaccines for inflammatory diseases such as Crohn's disease or comparison or Johne's disease in animals.

Sequence 262 Ä,

Query Match

Similarity

14.5%;

.9e-13 DB 18;

Length 262;

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                                                                                                                                                                                                              Matches
                                                    119
 179
                          176
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                                                                                                                                                                          RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQ-VAAFLGDHAASHLV 119
 EFILRA---
                        DFNIRCFSNPALITRYMDV--VISEYNDMTG
                                                  WGFGMDRLVGLDRVRGPIPFSLRKFLAGKQVVPHQASFFGSSLVAKIGGYDLDFGIAADQ
                                                                           YG---DVVMRSTKSRHAGPFDLDRLLFETNLC-HQSIFYRRELFDGIGPYNLRYRVWADW 175
                                                                                                     --YWQSEPDGGRYDAMNQGIAHASGDLLWFLHSADRFSGPDVVAQAVEALSGKGPVSEL-
                                                                                                                                                         SAPTVSVITISFNDLDGLQRTVKSVRAQRYRGRIEHIVIDGGSGDDVVAYLSGCEPGFA-
                                                                                                                                                                                                            68;
                                                                                                                                                                                                              Conservative
ALVCEPVTIRCVLCEF-DTTG
                                                                                                                                                                                                           ; Score 202.5;
; Pred. No. 1.9e
36; Mismatches
204
                        204
                                                                                                                                                                                                              90;
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                                                                                                                                                                                                           17; Gaps
                                                                                                                                                                                   60
                                                                                                                                                         61
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RESULT 6
AAW21779
ID AAW2

AAW21779 standard; Protein; 262

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                                                                                                                                                                                                                                        CC The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/BBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP26805
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                                                                                                                                    Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3429; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-352536/38
N-PSDB; ABN67436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                 Streptococcus proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-)
   64
                                    67
                                                                                                                                                   Local
                                                                                                     7
                                                                                SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
KNNGGLSDARNYGISRATGDYIYLLDSDDYLYKEDAIERMVEF-SEKYNSEIVLGCYVEK
                             GPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYG-----
                                                                 SIIIPVYNVQSFLNECIESVLAQTYSNLEIILVNDGSTDNSGDICD-YYSEIDGRIFVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIRON SPA.
INST GENOMIC RES
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                   321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-0026333.
2000GB-0028727.
2001GB-0005640.
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide SEQ
                                                                                                                                                  14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margarit Ros YI,
                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
                                                                                                                                Score 201.5; DB Pred. No. 3.4e-13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO
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                                                                                                                                63;
                                                                                                                                                              23;
                                                                                                                               Indels
                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser
                                                                                                                                                               321;
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                                                                                                                               Gaps
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AAW88314
AAW8814
AAW881
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                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 antigen;
diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O antigen. The use of nucleic acid molecules derived from particular assembly and transport genes, particularly wbd (transferase), wzx (flippase) and wzy (polymerase) genes, within O antigen gene clusters improves the specificity of methods for the detection and identification of O antigens, e.g. in testing foodor faecal-derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of a sugar transferase that is encoded by the wbdo open reading frame of a gene cluster (see AAX05749) involved in the biosynthesis of the Escherichia coli O157 O antigen. The use of nucleic acid molecules derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-059669/05
N-PSDB; AAX06749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 8; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigens - useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reeves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1997;
01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1999
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  100
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                                                    126 RSTKSRHAGPFDLDRLL-----FETNLCHQSIFYRRELFDGIGPYNLRYRVWADWDFN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 REQHIINIVLEDEMIETISPVQAIQNIYNYDAYRAIF--TVAHNKL-YKRELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                  60
                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                 7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVH- -65
KEPCLIKVGLFENDKLLGFSSITHSNTGYCHQGVIFPKNHSE----YDLRYKICADYKLI 155
                                                                                                                  YEKDEGIYDAMNKGRMLAKGDLIHYLNAGDSV---
                                                                                                                                                                    SGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVVM 125
                                                                                                                                                                                                                            SVITVTYNNAEGLEKTLSSLSILKIKPFEIIIVDGGSTDGTNRVISRFT----SMNITHV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR,
                                                                                                                                                                                                                                                                                                                                         67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or patient samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O157 antigen;
haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97AU-0008162.
97AU-0006545.
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                                                                                                                                                                                                                                                                                                                                                                       13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and haemorrhagic colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sugar transferase; wbdO gene;
colitis; diagnosis.
                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                         Score 190; DB 20;
Pred. No. 4.1e-12;
2; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for bacterial polysaccharide specific strains in, e.g. food,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                            ·IGD-----IYKNI--
                                                                                                                                                                                                                                                                                                                                                                                              Length 248;
                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                            99
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11;

Best Local Similarity

28.9%;

Pred.

No. 1.4e-11;

9;

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RESULT 9
AAY54072
ID AAY5
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                                                                                                                                                                                                                          AAY54065-74 represent enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and are encoded by open reading frames eps1-eps10. The enzymes are used from Streptococcus thermophilus strain Sfi39. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis
                            a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, EPS7 and EPS8 are beta-glycoxyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1998;
22-APR-1998;
22-APR-1998;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 105-106; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties fermented milk products -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS6; EPS7; EPS8; EPS9; EPS10; Streptococcus thermophilus strain Sfi3 activated D-galactose pyranose; saccharide; beta-qlycosyltransferase; transporter; food; fermented milk product; yoghurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY54072 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMFEKNKKN 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEVFPEG---LRSLSLITSGYVKYDMGGVSSKKRILRDKELAK---
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316
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B
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98EP-0201311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is involved in exopolysaccharide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamothe
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Query Match

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Score

186.5;

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RESULT 10
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Streptococcus thermophilus Sfi39. The operon contains 10 open reading frames, and encodes enzymes (eps1, eps2, eps3, eps4, eps5, eps6, eps7, eps8, eps9 and eps10) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between C1, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or probiotic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lartin activations.
                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eps operon; Streptococcus thermophilus Sfi39; en eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10; exopolysaccharide biosynthesis; EPS; intersugar
                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                             New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                           Stingele F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus thermophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of eps8 of Streptococcus thermophilus Sfi39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEP---TTLAQVAAFLGDHAASHLVY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             foodstuff;
l bacteria;
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98EP-0201311.
98EP-0201312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMRSTKSRHAGPFDLDRLLFETNLCH--OSIFYRRELFDGIGPYNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organoleptic quality; flavour; acidified milk product; yoghurt;
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                                                                                                                                                                                                                                                                                                                                                           Lamothe
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uality; flavour;
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RESULT 11
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      The present sequence represents a protein encoded by open reading frame (ORF) B of a novel polynucleotide sequence designated "GS". GS is a pathogenecity island of B kb of DNA comprising a core region of 5.75 kb with multiple ORFs and an adjacent transmissable element of 2.5 kb. The ORFs, and also the transmissable element, encode proteins which may be linked to pathogenecity, such as providing receptors for cellular recognition. GS was discovered and characterised using differential DNA analysis technology. It is found within Mycobacterium paratuberculosis
                                                                                                                                         New isolated pathogenicity island from mycobacteria - develop products for detection, diagnosis, prevention of mycobacteria infections
                                                                                                                                                                                                                                     Doran
                                                                                                                                                                                                                                                                                                                                                                                                      GS; pathogenecity island; pathogenic protein; mycobacterial cellular recognition receptor; pathogenic mycobacteria; Crol vaccine; inflammatory disease; sarcoidosis; Johne's disease
analysis technology. and it has also been
                                                                                                                                                                                                                           Sumar
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                                                                                                                    Claim 1;
                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
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DB; AAT74462.
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59; Conserv
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                                                                                                                   Page 45;
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                                                                                                                                                                                                                           Ford J, I
Tizard M;
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                                                                                                                                                                                                                                                            GEORGE'S HOSPITAL MEDICAL SCHOOL.
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                                                                                                                                                                                                                                                                                                                                                                                  subspecies
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Pred. No. 1.4e-11;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the intestine and Crohn's disease in humans. The protein products of ORFs of GS can be used for detecting mycobacteria or for diagnosing, treating or preventing mycobacterial disease. In particular they can used as vaccines for inflammatory diseases such as Crohn's disease or sarcoidosis in humans or Johne's disease in animals.
                          beauty cosmetics, comprises characteristics of Lactoc cremoris Ropy 352
                                                                                                                                                                        02-FEB-2000;
16-OCT-2000;
                                                                                                                                                                                                                                                                                                    EPS plasmid; Lactococcus lactis subspecies cremoris Ropy352; exopolysaccharide; EPS352; milk; thickener; glycosyltransferbiosynthesis; fruit juice.
                                                                                N-PSDB;
                                                                                         WPI; 2001-488889/53.
                                                                                                                                      (UYOR-)
                                                                                                                                                                                                          02-FEB-2001; 2001WO-US03404
                                                                                                                                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                                                                         W0200157234-A2
                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB47426 standard; Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      silvaticum.
                                                                                                                                                                                                                                                                                Lactococcus lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGRRVSW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WADWDFNIRCESNPALITR--YMDVVISEYNDMTGFSMRQGTDKEFR--KRL----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYGKNNLVGLDGKPLFPRPYGYMPFKMRKFLLGATVAHQATFFGASLVAKLGGYDLDFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G----DVVMRSTK---SRHAG--PFDLDRLLFETNLCHQSIFYRRELFDGIGPYNLRYRV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --YWQSQPDNGRYDAMNQGIAHSSGDLLWFMHSTDRFSDPDAVASVVEALSGHGPVRDLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVY 120
                                                                                                                JE,
                                                                                AAH43198
                                                                                                                                      UNIV OREGON STATE.
US DEPT OF AGRICUI
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                                                                                                               Knoshaug
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2000US-0241098.
                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                        AGRICULTURE
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27.3%;
                                                                                                                EP,
                                                                                                                Sandine
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Pred. No. 1.3e-11;
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                                                                                                                Ĕ,
                                                                                                              Ahlgren
                                                                                                                                                                                                                                                                                                                glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                JA,
                                              Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                Dierksen
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s lactis
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Claim 28; Page 67-68;

73pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS plasmid is about 32 kb in size and encodes at least 13 active genes. The enzymes encoded by these genes allow the bacteria to produce an exopolysaccharide, designated EPS352. When EPS352 is expressed in or added to milk, it imparts highly desirable sensory characteristics to the milk, including making the milk very thick, with a very smooth countries (ORF's) M and N show homology to glycosyltransferase involved in EPS352 is useful for thickering a liquid selected from thick, and he usba-has-NCAUR-NRL as deposited with the USDA-ARS-NCAUR-NRL as deposit accession number NRRL B-30229. EPS352 is useful for thickering a liquid selected from milk, a milk-based liquid, a whey-based liquid, a soy-based liquid, a milk-based liquid, a whey-based liquid, a soy-based liquid.
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Best Local
                                                                                                                                                                                                                                                                   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP26804 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           · 164 PYNLRYRVWADWDFNIRCFSNPALIT----RYMDVVISEYNDMTGFS------MRQG
 Telford J,
                                                                               27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                            WO200234771-A2
                                                                                                                                                                                                                                        Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2002
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                                                                                                                                             29-OCT-2001; 2001WO-GB04789
                                 (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 YNTKNIGVSHARNYGIDRASGSYIMFLDPDDT-YDKSYCLEMIGLINKFNA-----DVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDPEFYSQIDSVIFYNLVGWLITER----KSRENSQF-IRRNIKNMKSQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSNYYICKGKNIYPNVNNDLLECEGLLSRDKTMRSILSDTGFKGFVWTRIFRKNVINNV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 AA;
 Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                     polypeptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                   327
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                                                                                                                                                                                                                                                                                                                                      ID NO
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AAY68976
ID AAY66
AC AAY66
AC AAY66
AC AAY66
XX 30-M2
XX 20-M2
XX 20-M2
XX 20-M2
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated me meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of info or disease caused by Streptococcus bacteria, such as meningitis, for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 3429; 4525pp; English.
                                                                                                        30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus proteins.
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                                                                                                                                          AAY68976;
                                                                                                                                                                           AAY68976 standard;
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                                                                                                                                                                                                                                                                                                RLALRTRLIRVKAVSKER
                                                                                                                                                                                                                                                                                                                                -LYFFEAIQNNIVFINLNFPHNTSLISAVIYNEVFGGIDICGKMIDFKLYDTVDYYRKKY
                                                                                                                                                                                                                                                                                                                                                                  PMYFWVA----
                                                                                                                                                                                                                                                                                                                                                                                                   NLLSNPYPEGKIHEDMDTTFKLISCASKIA-VCDIVTA----VVYFSDNSTTRTKFNERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTS----IGNFUNTYNTSINSQYLKEIKLYTLEVALEEMYYGKTY--GVSPLAKLYPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLYEPTTLAQVAAFLGDHAASHLVYGDVV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to a protein (ABP25413-ABP30895)
                                                                                                                                                                                                                                                                                                                                                                                                                                   RVWADWDFNIRCFSNPALITRYMDVVISEYNDMTGFSMRQGTDKEFRKRL
                                                                                                                                                                           Protein;
                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.9%;
22.6%;
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                                                                                                                                                                            278
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                                                                                                                                                                                                                                                                                                                                                                 -GWETCRRMLAF-LKD----KENR
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13;

Capsular gene cluster; serotype 1; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection;

Cps1K

protein

which

has glycosyltransferase activity.

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RESULT 15
AAY68963
ID AAY68
XX
AC AAY68
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                   AAY68963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. against S. suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene cluster is used as a source of probes and primers for serotype-specific detection of S. suls and is also useful i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (Cps1E, Cps1G, Cps1I, Cps1I), Cps1K) and CP polymerase activities (Cps1H). The capsule confers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The proteins AAY68970-76 are encoded by the capsular gene cluster of Streptococcus suis serotype 1. The genes in this cluster are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-195104/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; vaccine; Streptococcal disease; Cps1E; Cps1F; Cps1G;
Cps1H; Cps1I; Cps1J; Cps1K; glycosyltransferase; CP polymerase.
                                                                           AAY68963 standard; Protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant production of the proteins. for producing antigens that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium resistance to complement-mediated opsonophagocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutants for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIEN-) STICHTING DIENST LANDBOUWKUNDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200005378-A2
                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                     171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eradicating a Streptococcal disease,
                                                                                                                                                                                                                                        TDKEF---
                                                                                                                                                                                                                                                                                                                                                                                                                 LGDHAASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC-----HQSI-----FYRR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVVHSGPDDGPYDAMNRGVGVATGEWVLFLGADDTLY------EPTTLAQVAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISKISIIVPIYNVEKYLSKCIDSIVNQTYKHIEILLVNDGSTDNSEEICLAYAKK-DSR
                                                                                                                                                                                         TDHRFHCLLEFQNERMDFY
                                                                                                                                                                                                                                                                              ELFE-----DFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDRENSITTSSM---
                                                                                                                                                                                                                                                                                                                        ELFDGIGPYNLRY---RVWADWDFNIRC---FSNPALITRYMDVVISEYNDMTGFSMRQG
                                                                                                                                                                                                                                                                                                                                                                     DRVDASGHELTAEPLPTN-------QAVLSGRNVCKKLLEADGHREVVACNKLYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRYFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAPVFSIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ60930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 4; 144pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                   ----RKRLPMY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98EP-0202465.
98EP-0202467.
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23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 179; DB 21; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in vaccines,
in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The proteins are then useful in vaccines, for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONDERZOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus suits serotype 2. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsA), chain length determination (CpsB, CpsC), export (CpsC), and biosynthesis (CpsE, CpsF, CpsG, CpsH, CpsJ, CpsK). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producting antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; ORF 2Z; ORF 2Z; ORF 2Z; ORF 2Z; Cps2B; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The proteins AAY68950-69 are encoded by the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-195104/17.
N-PSDB; AAZ60929.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cps2A; Cps2B;
Cps2K; Cps2O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cps2K protein which has glycosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capsular gene cluster; serotype 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
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                                                                                                                                          162
                                                                                                                                                                                    124
                                                                                                                                                                                                                                 115
    225
                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                                                                                          7 SIIIPTFNAAVTLQACLGSIVGQTYREVEVVLVDGGSTDRTLDIANSFRPELGSRLVVHS 66
                                                                                                                                                                                                                                                                       KENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDRVDA 123
                                                                                                                                                                                                                                                                                                                                                                SIIVPIXNVEQXLSKCINSIVNQTXKHIEILLVNDGSTDNSEEICLAYAKK-DSRIRYFK 63
HCLLEFQNERMDFYESRGDKELLLECYRSFLAFAVLFLGKYNHWLSKQQ--KKLLQTLFR
                                                 -----RKRLPMY---
                                                                                             ----DFRFEKGKIHEDEYFTYRLLYELEKVAIVKECLYYYVDRENSIITSSM---
                                                                                                                                     IGPYNLRY---RVWADWDFNIRC---FSNPALITRYMDVVISEYNDMTGFSMRQGTDKEF
                                                                                                                                                                                       SGHFLTAEPLPTN-----
                                                                                                                                                                                                                            ASHLVYGDVVMRSTKSRHAGPFDLDRLLFETNLC-----HQSI-----FYRRELFDG
                                                                                                                                                                                                                                                                                                                   GPDDGPYDAMNRGVGVATGEWVLFLGADDTLY-----EPTTLAQVAAFLGDHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cps2P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
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98EP-0202467
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; Cps2Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%;
                                                                                                                                                                                ----QAVLSGRNVCKKLLEADGHRFVVAWNKLYKKELFE- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 175; DB 21;
Pred. No. 2.7e-10;
7; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polysaccharide biosynthesis;
                                              -- FWVAGWETCRRML----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334;
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94;

Gaps

13;

IDHRF

224

215

161

282

망 236 -AFLKDKENRRLAL 248 : |:|:|||| 283 IVYKQLKQNKRLAL 296

Search completed: April 17, 2003, 17:26:56 Job time: 77 secs